

0590
10/8

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/039,761

DATE: 10/24/2002
TIME: 15:24:25

Input Set : A:\A70224.ST25.txt
Output Set: N:\CRF4\10242002\J039761.raw

3 <110> APPLICANT: Zhou, Xiula X. Z.
5 <120> TITLE OF INVENTION: MODULATORS OF LEUKOCYTE ACTIVATION, COMPOSITIONS AND METHODS
OF USE

7 <130> FILE REFERENCE: A-70224/RMS/DHR
9 <140> CURRENT APPLICATION NUMBER: US 10/039,761

C--> 10 <141> CURRENT FILING DATE: 2002-10-15
12 <150> PRIOR APPLICATION NUMBER: US 60/280,698
13 <151> PRIOR FILING DATE: 2001-03-29
15 <160> NUMBER OF SEQ ID NOS: 5
17 <170> SOFTWARE: PatentIn version 3.1

19 <210> SEQ ID NO: 1
20 <211> LENGTH: 3955
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
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25 <221> NAME/KEY: misc_feature
26 <222> LOCATION: (1473)..(1473)
27 <223> OTHER INFORMATION: "n" at position 1473 can be any base.
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31 <221> NAME/KEY: CDS
32 <222> LOCATION: (355)..(3522)
33 <223> OTHER INFORMATION:

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41 ccgcgtggag acgtgaggcg gccgcccgtg ccctcacagt cggcgtttcg ccgcctgccc 180
43 gcgggtgcccg cgcacgcctg ccgccatcgc cttcgcgcct ggctggcggg ggcgctgtcc 240
45 tcccaggccg tccgcgccgc tccctggagc tcggcgagc gcggcagcca gggccggcgg 300
47 aggcgcgagg agccgggccc caccgccgcc gccgcccgcg ccgccgcggg ggcc atg 357
48 Met
49 1
51 acc gtg gag cag aac gtg ctg cag cag agc gcg gcg cag aag cac cag 405
52 Thr Val Glu Gln Asn Val Leu Gln Gln Ser Ala Ala Gln Lys His Gln
53 5 10 15
55 cag acg ttt ttg aat caa ctg aga gaa att acg ggg att aat gac acc 453
56 Gln Thr Phe Leu Asn Gln Leu Arg Glu Ile Thr Gly Ile Asn Asp Thr
57 20 25 30
59 cag ata cta cag caa gcc ttg aag gat agt aat gga aac ttg gaa tta 501
60 Gln Ile Leu Gln Gln Ala Leu Lys Asp Ser Asn Gly Asn Leu Glu Leu
61 35 40 45
63 gca gtg gct ttc ctt act gcg aag aat gct aag acc cct cag cag gag 549
64 Ala Val Ala Phe Leu Thr Ala Lys Asn Ala Lys Thr Pro Gln Gln Glu
65 50 55 60 65
67 gag aca act tac tac caa aca gca ctt cct ggc aat gat aga tac atc 597

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71 agt gtg gga agc caa gca gat aca aat gtg att gat ctc act gga gat      645
72 Ser Val Gly Ser Gln Ala Asp Thr Asn Val Ile Asp Leu Thr Gly Asp
73                               85                               90                               95
75 gat aaa gat gat ctt cag aga aca att gcc ttg agt ttg gcc gaa tca      693
76 Asp Lys Asp Asp Leu Gln Arg Thr Ile Ala Leu Ser Leu Ala Glu Ser
77                               100                              105                              110
79 aac agg gca ttc agg gag act gga ata act gat gag gaa caa gcc att      741
80 Asn Arg Ala Phe Arg Glu Thr Gly Ile Thr Asp Glu Glu Gln Ala Ile
81                               115                              120                              125
83 agc aga gtt ctt gaa gcc agt ata gca gag aat aaa gca tgt ttg aag      789
84 Ser Arg Val Leu Glu Ala Ser Ile Ala Glu Asn Lys Ala Cys Leu Lys
85 130                               135                               140                               145
87 agg aca cct aca gaa gtt tgg agg gat tct cga aac cct tat gat aga      837
88 Arg Thr Pro Thr Glu Val Trp Arg Asp Ser Arg Asn Pro Tyr Asp Arg
89                               150                              155                              160
91 aaa aga cag gac aaa gct ccc gtt ggg cta aag aat gtt ggc aat act      885
92 Lys Arg Gln Asp Lys Ala Pro Val Gly Leu Lys Asn Val Gly Asn Thr
93                               165                              170                              175
95 tgt tgg ttt agt gct gtt att cag tca tta ttt aat ctt ttg gaa ttt      933
96 Cys Trp Phe Ser Ala Val Ile Gln Ser Leu Phe Asn Leu Leu Glu Phe
97                               180                              185                              190
99 aga aga tta gtt ctg aat tac aag cct cca tca aat gct caa gat tta      981
100 Arg Arg Leu Val Leu Asn Tyr Lys Pro Pro Ser Asn Ala Gln Asp Leu
101                               195                              200                              205
103 ccc cga aac caa aag gaa cat cgg aat ttg cct ttt atg cgt gag ctg      1029
104 Pro Arg Asn Gln Lys Glu His Arg Asn Leu Pro Phe Met Arg Glu Leu
105 210                               215                               220                               225
107 agg tat cta ttt gca ctt ctt gtt ggt acc aaa agg aag tat gtt gat      1077
108 Arg Tyr Leu Phe Ala Leu Leu Val Gly Thr Lys Arg Lys Tyr Val Asp
109                               230                              235                              240
111 cca tca aga gca gtt gaa att ctt aag gat gct ttc aaa tca aat gac      1125
112 Pro Ser Arg Ala Val Glu Ile Leu Lys Asp Ala Phe Lys Ser Asn Asp
113                               245                              250                              255
115 tca cag cag caa gat gtg agt gag ttt aca cac aaa tta tta gat tgg      1173
116 Ser Gln Gln Gln Asp Val Ser Glu Phe Thr His Lys Leu Leu Asp Trp
117                               260                              265                              270
119 tta gaa gat gcc ttc caa atg aaa gct gaa gag gag acg gat gaa gag      1221
120 Leu Glu Asp Ala Phe Gln Met Lys Ala Glu Glu Glu Thr Asp Glu Glu
121                               275                              280                              285
123 aag cca aag aac ccc atg gta gag ttg ttc tat ggc aga ttc ctg gct      1269
124 Lys Pro Lys Asn Pro Met Val Glu Leu Phe Tyr Gly Arg Phe Leu Ala
125 290                               295                               300                               305
127 gtg gga gta ctt gaa ggt aaa aaa ttt gaa aac act gaa atg ttt ggt      1317
128 Val Gly Val Leu Glu Gly Lys Lys Phe Glu Asn Thr Glu Met Phe Gly
129                               310                              315                              320
131 cag tac cca ctt cag gtc aat ggg ttc aaa gat ctg cat gag tgc cta      1365
132 Gln Tyr Pro Leu Gln Val Asn Gly Phe Lys Asp Leu His Glu Cys Leu

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133          325          330          335
135 gaa gct gca atg att gaa gga gaa att gag tct tta cat tca gag aat      1413
136 Glu Ala Ala Met Ile Glu Gly Glu Ile Glu Ser Leu His Ser Glu Asn
137          340          345          350
139 tca gga aaa tca ggc caa gag cat tgg ttt act gga tta cca cct gtg      1461
140 Ser Gly Lys Ser Gly Gln Glu His Trp Phe Thr Gly Leu Pro Pro Val
141          355          360          365
W--> 143 tta aca ttt gan ttg tca aga ttt gaa ttt aat cag gca ttg gga aga      1509
W--> 144 Leu Thr Phe Xaa Leu Ser Arg Phe Glu Phe Asn Gln Ala Leu Gly Arg
145 370          375          380          385
147 cca gaa aaa att cac aac aaa tta gaa ttt ccc caa gtt tta tat ttg      1557
148 Pro Glu Lys Ile His Asn Lys Leu Glu Phe Pro Gln Val Leu Tyr Leu
149          390          395          400
151 gac aga tac atg cac aga aac aga gaa ata aca aga att aag agg gaa      1605
152 Asp Arg Tyr Met His Arg Asn Arg Glu Ile Thr Arg Ile Lys Arg Glu
153          405          410          415
155 gag atc aag aga ctg aaa gat tac ctc acg gta tta caa caa agg cta      1653
156 Glu Ile Lys Arg Leu Lys Asp Tyr Leu Thr Val Leu Gln Gln Arg Leu
157          420          425          430
159 gaa aga tat tta agc tat ggt tcc ggt ccc aaa cga ttc ccc ttg gta      1701
160 Glu Arg Tyr Leu Ser Tyr Gly Ser Gly Pro Lys Arg Phe Pro Leu Val
161          435          440          445
163 gat gtt ctt cag tat gca ttg gaa ttt gcc tca agt aaa cct gtt tgc      1749
164 Asp Val Leu Gln Tyr Ala Leu Glu Phe Ala Ser Ser Lys Pro Val Cys
165 450          455          460          465
167 act tct cct gtt gac gat att gac gct agt tcc cca cct agt ggt tcc      1797
168 Thr Ser Pro Val Asp Asp Ile Asp Ala Ser Ser Pro Pro Ser Gly Ser
169          470          475          480
171 ata cca tca cag aca tta cca agc aca aca gaa caa cag gga gcc cta      1845
172 Ile Pro Ser Gln Thr Leu Pro Ser Thr Thr Glu Gln Gln Gly Ala Leu
173          485          490          495
175 tct tca gaa ctg cca agc aca tca cct tca tca gtt gct gcc att tca      1893
176 Ser Ser Glu Leu Pro Ser Thr Ser Pro Ser Ser Val Ala Ala Ile Ser
177          500          505          510
179 tcg aga tca gta ata cac aaa cca ttt act cag tcc cgg ata cct cca      1941
180 Ser Arg Ser Val Ile His Lys Pro Phe Thr Gln Ser Arg Ile Pro Pro
181          515          520          525
183 gat ttg ccc atg cat ccg gca cca agg cac ata acg gag gaa gaa ctt      1989
184 Asp Leu Pro Met His Pro Ala Pro Arg His Ile Thr Glu Glu Glu Leu
185 530          535          540          545
187 tct gtg ctg gaa agt tgt tta cat cgc tgg agg aca gaa ata gaa aat      2037
188 Ser Val Leu Glu Ser Cys Leu His Arg Trp Arg Thr Glu Ile Glu Asn
189          550          555          560
191 gac acc aga gat ttg cag gaa agc ata tcc aga atc cat cga aca att      2085
192 Asp Thr Arg Asp Leu Gln Glu Ser Ile Ser Arg Ile His Arg Thr Ile
193          565          570          575
195 gaa tta atg tac tct gac aaa tct atg ata caa gtt cct tat cga tta      2133
196 Glu Leu Met Tyr Ser Asp Lys Ser Met Ile Gln Val Pro Tyr Arg Leu
197          580          585          590

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199	cat	gcc	gtt	tta	gtt	cac	gaa	ggc	caa	gct	aat	gct	ggg	cac	tac	tgg	2181
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201		595					600					605					
203	gca	tat	att	ttt	gat	cat	cgt	gaa	agc	aga	tgg	atg	aag	tac	aat	gat	2229
204	Ala	Tyr	Ile	Phe	Asp	His	Arg	Glu	Ser	Arg	Trp	Met	Lys	Tyr	Asn	Asp	
205	610					615					620					625	
207	att	gct	gtg	aca	aaa	tca	tca	tgg	gaa	gag	cta	gtg	agg	gac	tct	ttt	2277
208	Ile	Ala	Val	Thr	Lys	Ser	Ser	Trp	Glu	Glu	Leu	Val	Arg	Asp	Ser	Phe	
209					630						635				640		
211	ggt	ggt	tat	aga	aat	gcc	agt	gca	tac	tgt	tta	atg	tac	ata	aat	gat	2325
212	Gly	Gly	Tyr	Arg	Asn	Ala	Ser	Ala	Tyr	Cys	Leu	Met	Tyr	Ile	Asn	Asp	
213				645					650					655			
215	aag	gca	cag	ttc	cta	ata	caa	gag	gag	ttt	aat	aaa	gaa	act	ggg	cag	2373
216	Lys	Ala	Gln	Phe	Leu	Ile	Gln	Glu	Glu	Phe	Asn	Lys	Glu	Thr	Gly	Gln	
217			660					665					670				
219	ccc	ctt	gtt	ggt	ata	gaa	aca	tta	cca	ccg	gat	ttg	aga	gat	ttt	gtt	2421
220	Pro	Leu	Val	Gly	Ile	Glu	Thr	Leu	Pro	Pro	Asp	Leu	Arg	Asp	Phe	Val	
221		675					680					685					
223	gag	gaa	gac	aac	caa	cga	ttt	gaa	aaa	gaa	cta	gaa	gaa	tgg	gat	gca	2469
224	Glu	Glu	Asp	Asn	Gln	Arg	Phe	Glu	Lys	Glu	Leu	Glu	Glu	Trp	Asp	Ala	
225	690					695					700					705	
227	caa	ctt	gcc	cag	aaa	gct	ttg	cag	gaa	aag	ctt	tta	gcg	tct	cag	aaa	2517
228	Gln	Leu	Ala	Gln	Lys	Ala	Leu	Gln	Glu	Lys	Leu	Leu	Ala	Ser	Gln	Lys	
229				710							715				720		
231	ttg	aga	gag	tca	gag	act	tct	gtg	aca	aca	gca	caa	gca	gca	gga	gac	2565
232	Leu	Arg	Glu	Ser	Glu	Thr	Ser	Val	Thr	Thr	Ala	Gln	Ala	Ala	Gly	Asp	
233				725					730					735			
235	cca	gaa	tat	cta	gag	cag	cca	tca	aga	agt	gat	ttc	tca	aag	cac	ttg	2613
236	Pro	Glu	Tyr	Leu	Glu	Gln	Pro	Ser	Arg	Ser	Asp	Phe	Ser	Lys	His	Leu	
237		740					745						750				
239	aaa	gaa	gaa	act	att	caa	ata	att	acc	aag	gca	tca	cat	gag	cat	gaa	2661
240	Lys	Glu	Glu	Thr	Ile	Gln	Ile	Ile	Thr	Lys	Ala	Ser	His	Glu	His	Glu	
241		755				760					765						
243	gat	aaa	agt	cct	gaa	aca	gtt	ttg	cag	tcg	gca	att	aag	ttg	gaa	tat	2709
244	Asp	Lys	Ser	Pro	Glu	Thr	Val	Leu	Gln	Ser	Ala	Ile	Lys	Leu	Glu	Tyr	
245	770					775					780				785		
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248	Ala	Arg	Leu	Val	Lys	Leu	Ala	Gln	Glu	Asp	Thr	Pro	Pro	Glu	Thr	Asp	
249				790							795				800		
251	tat	cgt	tta	cat	gta	gtg	gtc	tac	ttt	atc	cag	aac	cag	gca	cca		2805
252	Tyr	Arg	Leu	His	Val	Val	Val	Tyr	Phe	Ile	Gln	Asn	Gln	Ala	Pro		
253				805				810					815				
255	aag	aaa	att	att	gag	aaa	aca	tta	cta	gaa	caa	ttt	gga	gat	aga	aat	2853
256	Lys	Lys	Ile	Ile	Glu	Lys	Thr	Leu	Leu	Glu	Gln	Phe	Gly	Asp	Arg	Asn	
257		820					825					830					
259	ttg	agt	ttt	gat	gaa	agg	tgt	cac	aac	ata	atg	aaa	gtt	gct	caa	gcc	2901
260	Leu	Ser	Phe	Asp	Glu	Arg	Cys	His	Asn	Ile	Met	Lys	Val	Ala	Gln	Ala	
261		835				840					845						
263	aaa	ctg	gaa	atg	ata	aaa	cct	gaa	gaa	gta	aac	ttg	gag	gaa	tat	gag	2949

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268 Glu Trp His Gln Asp Tyr Arg Lys Phe Arg Glu Thr Thr Met Tyr Leu
269 870 875 880
271 ata att ggg cta gaa aat ttt caa aga gaa agt tat ata gat tcc ttg 3045
272 Ile Ile Gly Leu Glu Asn Phe Gln Arg Glu Ser Tyr Ile Asp Ser Leu
273 885 890 895
275 ctg ttc ctc atc tgt gct tat cag aat aac aaa gaa ctc ttg tct aaa 3093
276 Leu Phe Leu Ile Cys Ala Tyr Gln Asn Asn Lys Glu Leu Leu Ser Lys
277 900 905 910
279 ggc tta tac aga gga cat gat gaa gaa ttg ata tca cat tat aga aga 3141
280 Gly Leu Tyr Arg Gly His Asp Glu Glu Leu Ile Ser His Tyr Arg Arg
281 915 920 925
283 gaa tgt ttg cta aaa tta aat gag caa gcc gca gaa ctc ttc gaa tct 3189
284 Glu Cys Leu Leu Lys Leu Asn Glu Gln Ala Ala Glu Leu Phe Glu Ser
285 930 935 940 945
287 gga gag gat cga gaa gta aac aat ggt ttg att atc atg aat gag ttt 3237
288 Gly Glu Asp Arg Glu Val Asn Asn Gly Leu Ile Ile Met Asn Glu Phe
289 950 955 960
291 att gtc cca ttt ttg cca tta tta ctg gtg gat gaa atg gaa gaa aag 3285
292 Ile Val Pro Phe Leu Pro Leu Leu Val Asp Glu Met Glu Glu Lys
293 965 970 975
295 gat ata cta gct gta gaa gat atg aga aat cga tgg tgt tcc tac ctt 3333
296 Asp Ile Leu Ala Val Glu Asp Met Arg Asn Arg Trp Cys Ser Tyr Leu
297 980 985 990
299 ggt caa gaa atg gaa cca cac ctc caa gaa aag ctg aca gat ttt ttg 3381
300 Gly Gln Glu Met Glu Pro His Leu Gln Glu Lys Leu Thr Asp Phe Leu
301 995 1000 1005
303 cca aaa ctg ctt gat tgt tct atg gag att aaa agt ttc cat gag 3426
304 Pro Lys Leu Leu Asp Cys Ser Met Glu Ile Lys Ser Phe His Glu
305 1010 1015 1020
307 cca ccg aag tta cct tca tat tcc acg cat gaa ctc tgt gag cga 3471
308 Pro Pro Lys Leu Pro Ser Tyr Ser Thr His Glu Leu Cys Glu Arg
309 1025 1030 1035
311 ttt gcc cga atc atg ttg tcc ctc agt cga act cct gct gat gga 3516
312 Phe Ala Arg Ile Met Leu Ser Leu Ser Arg Thr Pro Ala Asp Gly
313 1040 1045 1050
315 aga taa actgcacact ttccctgaac acactgtata aactcttttt agttcttaac 3572
316 Arg
317 1055
319 ccttgccctc ctgtcacagg gtttgcttgt tgctgctata gtttttaact tttttttatt 3632
321 ttaataactg caaaagacaa aatgactata cagacttttag tcagactgca gacaataaag 3692
323 ctgaaaatcg catggcgtc agacatttta accggaactg atgtataatc acaaactctaa 3752
325 ttgattttat tatggcaaaa ctatgctttt gccaccttcc tgttgagta ttactttgct 3812
327 tttatctttt ctttctcaac agctttccat tcagtctgga tccttccatg actacagcca 3872
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331 aataaagttt tatttatggc tac 3955
334 <210> SEQ ID NO: 2

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/039,761

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 1473
Seq#:1; Xaa Pos. 373
Seq#:2; Xaa Pos. 373
Seq#:3; N Pos. 1473
Seq#:3; Xaa Pos. 373
Seq#:4; Xaa Pos. 373

VERIFICATION SUMMARY

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Input Set : A:\A70224.ST25.txt

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L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:36 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:33
L:143 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:1461
L:144 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:1509
L:443 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:368
L:636 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:633
L:743 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:1461
L:744 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:1509
L:1047 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:368